

241421.txt
SEQUENCE LISTING

<110> Sewalt, Vincent
Hastings, Craig
Meeley, Robert
Hantke, Sabine
Jung, Rudolf
Everard, John
Allen, Stephen

<120> COMPOSITIONS AND METHODS FOR ALTERING THE DISULFIDE STATUS OF PROTEINS

<130> 5718-119 (035718/241421)

<150> 60/250,703
<151> 2000-12-01

<160> 25

<170> PatentIn version 3.0

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<211> 797
<212> DNA
<213> Zea mays

<220>
<221> CDS
<222> (187)..(573)

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tgattatttc taggaaacac atgccgaaat gagggcacca ttatccgcgt ccagtgtgtc
120

cgctactccg ctccccctca gtcctcagtt cctcacctag cggttagcgtg cgcgccggag
180

acgttag atg gcg gct tcg gag gcg gca gcg gcg gca aca ccg gtg
228

Met Ala Ala Ser Glu Ala Ala Ala Ala Ala Ala Thr Pro Val
1 5 10

acg ccg aca gag ggg acg gtg atc gcg atc cac agc ctg gag gag tgg
276

Thr Pro Thr Glu Gly Thr Val Ile Ala Ile His Ser Leu Glu Glu Trp
15 20 25 30

agc atc cag atc gag gag gcc aac agc gcc aag aag ctg gtg gtg att
324

Ser Ile Gln Ile Glu Glu Ala Asn Ser Ala Lys Lys Leu Val Val Ile
35 40 45

gac ttc act gca aca tgg tgt cct ccg tgc cgc gcc atg gct cca att
372

Asp Phe Thr Ala Thr Trp Cys Pro Pro Cys Arg Ala Met Ala Pro Ile

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50

55

60

ttt gct gat atg gcc aag aag tcc cca aat gtt gtt ttc ctg aaa gtt
420
Phe Ala Asp Met Ala Lys Lys Ser Pro Asn Val Val Phe Leu Lys Val
65 70 75

gat gtg gat gaa atg aag acc att gct gag caa ttc agc gta gag gcc
468
Asp Val Asp Glu Met Lys Thr Ile Ala Glu Gln Phe Ser Val Glu Ala
80 85 90

atg cca aca ttc ctg ttc atg agg gag ggc gac gtc aag gac agg gtc
516
Met Pro Thr Phe Leu Phe Met Arg Glu Gly Asp Val Lys Asp Arg Val
95 100 105 110

gtt ggc gca gca aag gaa gag cta gca agg aag ctt gaa cta cac atg
564
Val Gly Ala Ala Lys Glu Glu Leu Ala Arg Lys Leu Glu Leu His Met
115 120 125

gcc tcg tag atcagtatgc cgtaatgtatgttgcct aaataagagg
613
Ala Ser

acgcctcgcc tcaactctga gaaaactagt gcttctgtga tggtaattcg tatgagagag
673

tgcccccttt ggtggtaactt cttcgtatgt agtattaactt cctgtcttaa tatgttgccc
733

aaaaa
797

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<212> PRT
<213> Zea mays

<400> 2

Met	Ala	Ala	Ser	Glu	Ala	Thr	Pro	Val	Thr	Pro						
1				5					10					15		

Thr Glu Gly Thr Val Ile Ala Ile His Ser Leu Glu Glu Trp Ser Ile
20 25 30

Gln Ile Glu Glu Ala Asn Ser Ala Lys Lys Leu Val Val Ile Asp Phe
35 40 45

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Thr Ala Thr Trp Cys Pro Pro Cys Arg Ala Met Ala Pro Ile Phe Ala
50 55 60

Asp Met Ala Lys Lys Ser Pro Asn Val Val Phe Leu Lys Val Asp Val
65 70 75 80

Asp Glu Met Lys Thr Ile Ala Glu Gln Phe Ser Val Glu Ala Met Pro
85 90 95

Thr Phe Leu Phe Met Arg Glu Gly Asp Val Lys Asp Arg Val Val Gly
100 105 110

Ala Ala Lys Glu Glu Leu Ala Arg Lys Leu Glu Leu His Met Ala Ser
115 120 125

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<222> (69)...(455)

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60
agacgttag atg gct tcg gag gct gct gct gct gct gct gct aca ccg gtg
110
Met Ala Ala Ser Glu Ala Ala Ala Ala Ala Ala Thr Pro Val
1 5 10

gct ccg aca gag ggg acg gtg atc gct atc cac agc ctg gag gag tgg
158
Ala Pro Thr Glu Gly Thr Val Ile Ala Ile His Ser Leu Glu Glu Trp
15 20 25 30

agc atc cag atc gag gag gcc aac agc gcc aag aag ctg gtg gtg att
206
Ser Ile Gln Ile Glu Glu Ala Asn Ser Ala Lys Lys Leu Val Val Ile
35 40 45

gac ttc act gca aca tgg tgt cct ccg tgc cgc gcc atg gct cca att
254
Asp Phe Thr Ala Thr Trp Cys Pro Pro Cys Arg Ala Met Ala Pro Ile
50 55 60

ttt gct gat atg gcc aag aag tcc cca aat gtt gtt ttc ctg aaa gtt
302
Phe Ala Asp Met Ala Lys Lys Ser Pro Asn Val Val Phe Leu Lys Val
65 70 75

gat gtc gat gaa atg aag acc att gct gag caa ttc agc gta gag gcc
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350

Asp Val Asp Glu Met Lys Thr Ile Ala Glu Gln Phe Ser Val Glu Ala
80 85 90

atg cca aca ttc ctg ttc atg agg gag ggc gac gtc aag gac agg gtc
398

Met Pro Thr Phe Leu Phe Met Arg Glu Gly Asp Val Lys Asp Arg Val
95 100 105 110

gtt ggc gca gca aag gaa gag cta gca agg aag ctt gaa cta cac atg
446

Val Gly Ala Ala Lys Glu Glu Leu Ala Arg Lys Leu Glu Leu His Met
115 120 125

gcc tcg tag atcagtgtatcgccatcgta gtattcgccct aaataagagg

495

Ala Ser

acgcctcgcc tcaactctga gaaaactagt gcttctgtga tggtaattcg tatgagagag
555

tgcccccttt ggtggactt ctgcgtatgt agtattaact cctgtcttaa tatgttgccc
615

tgcttgct tttcatacca tgtttgcctt ttcaagctgag gtgttatacg gtaaatcgga
675

gtcaatatct ttgaaattga ttaaaaaaaaaaaaaaa aaaaaaaaaaaaaaaa aaaaaaaaaaaaa
735

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795

aaaaa

799

<210> 4

<211> 128

<212> PRT

<213> Zea mays

<400> 4

Met Ala Ala Ser Glu Ala Ala Ala Ala Ala Ala Thr Pro Val Ala Pro
1 5 10 15

Thr Glu Gly Thr Val Ile Ala Ile His Ser Leu Glu Glu Trp Ser Ile
20 25 30

Gln Ile Glu Glu Ala Asn Ser Ala Lys Lys Leu Val Val Ile Asp Phe
35 40 45

Thr Ala Thr Trp Cys Pro Pro Cys Arg Ala Met Ala Pro Ile Phe Ala
50 55 60

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Asp Met Ala Lys Lys Ser Pro Asn Val Val Phe Leu Lys Val Asp Val
65 70 75 80

Asp Glu Met Lys Thr Ile Ala Glu Gln Phe Ser Val Glu Ala Met Pro
85 90 95

Thr Phe Leu Phe Met Arg Glu Gly Asp Val Lys Asp Arg Val Val Gly
100 105 110

Ala Ala Lys Glu Glu Leu Ala Arg Lys Leu Glu Leu His Met Ala Ser
115 120 125

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<212> DNA
<213> Zea mays

<220>
<221> CDS
<222> (3)..(194)

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47 Arg Phe Ser Asp Ala Ile Phe Val Lys Val Asp Val Asp Glu Leu
1 5 10 15

gct gag gtc gca agg aca tgg aag gta gag gct atg cca acg ttc gta
95 Ala Glu Val Ala Arg Thr Trp Lys Val Glu Ala Met Pro Thr Phe Val
20 25 30

ctt gtc aag gat ggg aag gag gta agc cgt gtg gtt ggg gcc aag aag
143 Leu Val Lys Asp Gly Lys Glu Val Ser Arg Val Val Gly Ala Lys Lys
35 40 45

gac gag ctt gag agg aag atc cgg atg ttc acg tca tct tcc tca tcg
191 Asp Glu Leu Glu Arg Lys Ile Arg Met Phe Thr Ser Ser Ser Ser
50 55 60

taa actcctgtgg ttgcgcctggg acggagttgc tgaagtgaaa tggcccttc
244

tctcaatgct gaaaaaaggg ggaaaaacta tgtaaaaatg atggtagacg tgtctgggtc
304

agtaataaga gtttctaaaa tctgaatgag atttgaatcg ctttccgttg ctgaaaaaaaa
364

aaa
367

<210> 6
 <211> 63
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 <213> Zea mays

 <400> 6

 Arg Phe Ser Asp Ala Ile Phe Val Lys Val Asp Val Asp Glu Leu Ala
 1 5 10 15

 Glu Val Ala Arg Thr Trp Lys Val Glu Ala Met Pro Thr Phe Val Leu
 20 25 30

 Val Lys Asp Gly Lys Glu Val Ser Arg Val Val Gly Ala Lys Lys Asp
 35 40 45

 Glu Leu Glu Arg Lys Ile Arg Met Phe Thr Ser Ser Ser Ser
 50 55 60

 <210> 7
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 <212> DNA
 <213> Zea mays

 <220>
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 Met Gly Ser Phe Phe Ser
 1 5

 acc tta gtg acg ccc cct ccg ccc gcc gcc gac gac ccg aac tgc gcc
 103
 Thr Leu Val Thr Pro Pro Pro Ala Ala Asp Asp Pro Asn Cys Ala
 10 15 20

 gtg gtg gcc gcg cac tcc aag gcc acc tac gac gag cag tgg gcg gcc
 151
 Val Val Ala Ala His Ser Lys Ala Thr Tyr Asp Glu Gln Trp Ala Ala
 25 30 35

 cac aag agc agc aag ctg atg gtg atc gac ttc tcg gcg tcc tgg
 199
 His Lys Ser Ser Ser Lys Leu Met Val Ile Asp Phe Ser Ala Ser Trp
 40 45 50

 tgc ggg ccc tgc cgc ttc atc gag ccg gcc ttc aag gag ctg gcc tcc
 247
 Cys Gly Pro Cys Arg Phe Ile Glu Pro Ala Phe Lys Glu Leu Ala Ser
 55 60 65 70

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cgc ttc acc gat gcc atc ttc atc aag gtc gac gtc gac gag ctc gcg
295 .
Arg Phe Thr Asp Ala Ile Phe Ile Lys Val Asp Val Asp Glu Leu Ala
75 80 85

gag gtc gca agg aca tgg aag gta gag gcg atg cca acg ttc gtg ctg
343
Glu Val Ala Arg Thr Trp Lys Val Glu Ala Met Pro Thr Phe Val Leu
90 95 100

gtc aag gat ggg aag gag gta ggc cgt gtg att ggg gct aag aag gac
391
Val Lys Asp Gly Lys Glu Val Gly Arg Val Ile Gly Ala Lys Lys Asp
105 110 115

gag ctt gag agg aag atc agg atg ttc gtc acg tca tct tcc tcg tcc
439
Glu Leu Glu Arg Lys Ile Arg Met Phe Val Thr Ser Ser Ser Ser
120 125 130

taa ctttagcagtg catacactcc caccttatta ctggttctc gactccagtg
492
gttcgcctgg gacggggttg ctgaaatggt tcccttctc gaatactgaa aaatcaaaaa
552

aagaagtata tgaaaaaatg atggtagacg tgtctggtc aataagagtt tctgaaactt
612

ggatttgtat gtgtcagtct ctgtgttctg tttccaagga atggatcatg tgagtttgg
672

atatactgg aaatatgtt tgctgttaaa aaaaaaaaaa aaaaaaaaa
720

<210> 8
<211> 134
<212> PRT
<213> Zea mays

<400> 8

Met Gly Ser Phe Phe Ser Thr Leu Val Thr Pro Pro Pro Pro Ala Ala
1 5 10 15

Asp Asp Pro Asn Cys Ala Val Val Ala Ala His Ser Lys Ala Thr Tyr
20 25 30

Asp Glu Gln Trp Ala Ala His Lys Ser Ser Ser Lys Leu Met Val Ile
35 40 45

Asp Phe Ser Ala Ser Trp Cys Gly Pro Cys Arg Phe Ile Glu Pro Ala
50 55 60

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Phe Lys Glu Leu Ala Ser Arg Phe Thr Asp Ala Ile Phe Ile Lys Val
65 70 75 80

Asp Val Asp Glu Leu Ala Glu Val Ala Arg Thr Trp Lys Val Glu Ala
85 90 95

Met Pro Thr Phe Val Leu Val Lys Asp Gly Lys Glu Val Gly Arg Val
100 105 110

Ile Gly Ala Lys Lys Asp Glu Leu Glu Arg Lys Ile Arg Met Phe Val
115 120 125

Thr Ser Ser Ser Ser Ser
130

<210> 9
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<213> Zea mays

<220>
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<222> (84)..(455)

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ccaccgagga agaagagaga gga atg gcg tcc gag gag gaa gga gtc gtg atc
113
Met Ala Ser Glu Glu Gly Val Val Ile
1 5 10

gcc tgc cac acc aag gcc gac ttc gac gcc cac atg gcc aag gcc aag
161
Ala Cys His Thr Lys Ala Asp Phe Asp Ala His Met Ala Lys Ala Lys
15 20 25

gag gcc ggc aag ctg gtg atc att gac ttc acg gcc tcc tgg tgc ggc
209
Glu Ala Gly Lys Leu Val Ile Ile Asp Phe Thr Ala Ser Trp Cys Gly
30 35 40

ccc tgc cgc ttc atc gcg cca ctg ttc gtc gag cac gcc aag aag ttc
257
Pro Cys Arg Phe Ile Ala Pro Leu Phe Val Glu His Ala Lys Lys Phe
45 50 55

acc cag gct gtg ttc ctg aag gtg gac gtg gac gag ctg aag gaa gtt
305
Thr Gln Ala Val Phe Leu Lys Val Asp Val Asp Glu Leu Lys Glu Val
60 65 70

1. CROSSING IN THE OLD

241421.txt
gcc gcg gcc tac gat gtc gag gcg atg ccg acc ttc cac ttc gtc aag
353
Ala Ala Ala Tyr Asp Val Glu Ala Met Pro Thr Phe His Phe Val Lys
75 80 85 90
aac ggg gtg acg gtc gag acc gtc gtc ggt gcc agg aag gag aac ctc
401
Asn Gly Val Thr Val Glu Thr Val Val Gly Ala Arg Lys Glu Asn Leu
95 100 105
ctg gcc cag atc gag aag cac tgc gcc gcg gcc gtg cct gct gcg tct
449
Leu Ala Gln Ile Glu Lys His Cys Ala Ala Ala Val Pro Ala Ala Ser
110 115 120
gcg tag agaggatgga ccagcacgtg gcgggtggcgg tggcggttgt ctgtcgttt
505
Ala
tcagtttggg ctgtcagct gtggctgggt ggttgattgt gaactggagc atgcagttt
565
actctgggag cccatcattt ggttggctca ggtgtcaata atctgtatac cttaatcatg
625
gatagttgtt gtgagttgtt attggacttt ggaatttggg tgtctggctt cgttctgtta
685
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722
<210> 10
<211> 123
<212> PRT
<213> Zea mays
<400> 10
Met Ala Ser Glu Glu Glu Gly Val Val Ile Ala Cys His Thr Lys Ala
1 5 10 15
Asp Phe Asp Ala His Met Ala Lys Ala Lys Glu Ala Gly Lys Leu Val
20 25 30
Ile Ile Asp Phe Thr Ala Ser Trp Cys Gly Pro Cys Arg Phe Ile Ala
35 40 45
Pro Leu Phe Val Glu His Ala Lys Lys Phe Thr Gln Ala Val Phe Leu
50 55 60
Lys Val Asp Val Asp Glu Leu Lys Glu Val Ala Ala Ala Tyr Asp Val
65 70 75 80

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Glu Ala Met Pro Thr Phe His Phe Val Lys Asn Gly Val Thr Val Glu
85 90 95

Thr Val Val Gly Ala Arg Lys Glu Asn Leu Leu Ala Gln Ile Glu Lys
100 105 110

His Cys Ala Ala Ala Val Pro Ala Ala Ser Ala
115 120

<210> 11
<211> 727
<212> DNA
<213> Zea mays

<220>
<221> CDS
<222> (84)..(452)

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cgacaccgag gaagaagaga tca atg gcg tcc gag cag gga gtc gtg atc gcg
113
Met Ala Ser Glu Gln Gly Val Val Ile Ala
1 5 10

tgc cac agc aag gct gag ttt gac gcc cac atg acc aag gcc cag gaa
161
Cys His Ser Lys Ala Glu Phe Asp Ala His Met Thr Lys Ala Gln Glu
15 20 25

gcc ggc aag ctg gtg gtc att gac ttc act gcc gcc tgg tgc ggt cca
209
Ala Gly Lys Leu Val Val Ile Asp Phe Thr Ala Ala Trp Cys Gly Pro
30 35 40

tgc cgc gcc atc gcc cca ctg ttc gtc gaa cac gcc aag aag ttc act
257
Cys Arg Ala Ile Ala Pro Leu Phe Val Glu His Ala Lys Lys Phe Thr
45 50 55

cag gtc gtc ttc ctg aag gtg gac gtg gac gaa gtg aag gaa gtc acc
305
Gln Val Val Phe Leu Lys Val Asp Val Asp Glu Val Lys Glu Val Thr
60 65 70

gct gcc tac gag gtc gag gct atg ccg acc ttc cac ttc gtc aag aac
353
Ala Ala Tyr Glu Val Glu Ala Met Pro Thr Phe His Phe Val Lys Asn
75 80 85 90

ggc aag acg gtc gct acc atc gtg ggt gcc aag aag gac gag ctc ctg
401
Gly Lys Thr Val Ala Thr Ile Val Gly Ala Lys Lys Asp Glu Leu Leu

Zea mays

241421.txt

95

100

105

gcc cag atc gag aag cat gcc gcg cct gcg cct gcg tct gcg tct gcc
449
Ala Gln Ile Glu Lys His Ala Ala Pro Ala Pro Ala Ser Ala Ser Ala
110 115 120

taa aggagatcg atcagtcgtc gccgtcaata agggccagca cgtatggctg
502

taaatgttgt cgttatcagt tctggcttg tcgttgtgg gcgattgtga actagtagta
562

tgtttgttgc tatccgagcc ggaggcgata cttaaccatg gatacttgtt gtgagttcgt
622

ttctgttcgc gtgtgactct tgaattgaat caaccagctc accactgcac caggccgtgg
682

tgagtggtga cagtgatttc ctgtaaaaaa aaaaaaaaaa aaaaa
727

<210> 12
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<212> PRT
<213> Zea mays

<400> 12

Met Ala Ser Glu Gln Gly Val Val Ile Ala Cys His Ser Lys Ala Glu
1 5 10 15

Phe Asp Ala His Met Thr Lys Ala Gln Glu Ala Gly Lys Leu Val Val
20 25 30

Ile Asp Phe Thr Ala Ala Trp Cys Gly Pro Cys Arg Ala Ile Ala Pro
35 40 45

Leu Phe Val Glu His Ala Lys Lys Phe Thr Gln Val Val Phe Leu Lys
50 55 60

Val Asp Val Asp Glu Val Lys Glu Val Thr Ala Ala Tyr Glu Val Glu
65 70 75 80

Ala Met Pro Thr Phe His Phe Val Lys Asn Gly Lys Thr Val Ala Thr
85 90 95

Ile Val Gly Ala Lys Lys Asp Glu Leu Leu Ala Gln Ile Glu Lys His
100 105 110

Ala Ala Pro Ala Pro Ala Ser Ala Ser Ala

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115 120

<210> 13
 <211> 700
 <212> DNA
 <213> Zea mays

<220>
 <221> CDS
 <222> (41)...(421)

<400> 13
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 55
 Met Ala Ala Glu Glu
 1 5

ggt gcc gtg atc gcg tgc cac acc aag gac gag ttc gac gcc cgc atg
 103
 Gly Ala Val Ile Ala Cys His Thr Lys Asp Glu Phe Asp Ala Arg Met
 10 15 20

gcc aag gcc aag gag cag ggc aag ctg gtg gtc atc gac ttc atg gcc
 151
 Ala Lys Ala Lys Glu Gln Gly Lys Leu Val Val Ile Asp Phe Met Ala
 25 30 35

ccc tgg tgc agt ggg tgc cag atg atg gcc ccg gtg tac gcg gac tgc
 199
 Pro Trp Cys Ser Gly Cys Gln Met Met Ala Pro Val Tyr Ala Asp Cys
 40 45 50

gcc agc aag tac cct tcc gcc gtc ttc ctc gag gtc gac gtc gac gaa
 247
 Ala Ser Lys Tyr Pro Ser Ala Val Phe Leu Glu Val Asp Val Asp Glu
 55 60 65

ctg ctg gaa gtc gcg aag atc tac ggc gtc cat gtg atg ccg acc ttc
 295
 Leu Leu Glu Val Ala Lys Ile Tyr Gly Val His Val Met Pro Thr Phe
 70 75 80 85

tgc ttc atc agg aac ggc gag acg ctc gag agc ttt gct acc gtc gac
 343
 Cys Phe Ile Arg Asn Gly Glu Thr Leu Glu Ser Phe Ala Thr Val Asp
 90 95 100

gag gac gag ctc cgg gac gcc gtc agg aag tac gac gcc gtc gac act
 391
 Glu Asp Glu Leu Arg Asp Ala Val Arg Lys Tyr Ala Ala Gly Thr
 105 110 115

acg acg gct cct gcc tcg gcg tcc gcc taa ttccaggat gtgtatgtta
 441
 Thr Thr Ala Pro Ala Ser Ala Ser Ala
 120 125

gcaaatagcg cgccgcacc agtcgtcaat aaataaataa ataaataaataa aaataaataa

501

ataaataaat aaaggccaac gtacgacgac aaatttagtgg cgcgcgcgtt agtagctagc
561

agagtatgcg ccgccactgt gtcgatctgc agtttggcg tttaaaagtg attttagtgt
621

gtactatgtt cagctcgaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa
681

aaaaaaaaaa aaaaaaaaaa
700

<210> 14
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<212> PRT
<213> Zea mays

<400> 14

Met Ala Ala Glu Glu Gly Ala Val Ile Ala Cys His Thr Lys Asp Glu
1 5 10 15

Phe Asp Ala Arg Met Ala Lys Ala Lys Glu Gln Gly Lys Leu Val Val
20 25 30

Ile Asp Phe Met Ala Pro Trp Cys Ser Gly Cys Gln Met Met Ala Pro
35 40 45

Val Tyr Ala Asp Cys Ala Ser Lys Tyr Pro Ser Ala Val Phe Leu Glu
50 55 60

Val Asp Val Asp Glu Leu Leu Glu Val Ala Lys Ile Tyr Gly Val His
65 70 75 80

Val Met Pro Thr Phe Cys Phe Ile Arg Asn Gly Glu Thr Leu Glu Ser
85 90 95

Phe Ala Thr Val Asp Glu Asp Glu Leu Arg Asp Ala Val Arg Lys Tyr
100 105 110

Ala Ala Ala Gly Thr Thr Ala Pro Ala Ser Ala Ser Ala
115 120 125

<210> 15
<211> 658
<212> DNA
<213> Hordeum vulgare

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<220>
 <221> CDS
 <222> (52)..(420)

<400> 15
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 57

Met Ala
1

gcg tcg gca acg gcg gca gtg gcg gcg gag gtg atc tcg gtc cac
 105
 Ala Ser Ala Thr Ala Ala Val Ala Ala Glu Val Ile Ser Val His
 5 10 15

agc ctg gag cag tgg acc atg cag atc gag gag gcc aac acc gcc aag
 153
 Ser Leu Glu Gln Trp Thr Met Gln Ile Glu Glu Ala Asn Thr Ala Lys
 20 25 30

aag ctg gtg gtg att gac ttc act gca tca tgg tgc gga cca tgc cgc
 201
 Lys Leu Val Val Ile Asp Phe Thr Ala Ser Trp Cys Gly Pro Cys Arg
 35 40 45 50

atc atg gct cca gtt ttc gct gat ctc gcc aag aag ttc cca aat gct
 249
 Ile Met Ala Pro Val Phe Ala Asp Leu Ala Lys Lys Phe Pro Asn Ala
 55 60 65

gtt ttc ctc aag gtc gac gtg gat gaa ctg aag ccc att gct gag caa
 297
 Val Phe Leu Lys Val Asp Val Asp Glu Leu Lys Pro Ile Ala Glu Gln
 70 75 80

ttc agt gtc gag gcc atg cca acg ttc ctg ttc atg aag gaa gga gac
 345
 Phe Ser Val Glu Ala Met Pro Thr Phe Leu Phe Met Lys Glu Gly Asp
 85 90 95

gtc aag gac agg gtt gtc gga gct atc aag gag gaa ctg acc gcc aag
 393
 Val Lys Asp Arg Val Val Gly Ala Ile Lys Glu Glu Leu Thr Ala Lys
 100 105 110

gtt ggg ctt cac gcg gcc cag taa ttacctattt gtgttagtatt
 440
 Val Gly Leu His Ala Ala Gln
 115 120

cgcctaaata aaattgccgc tcaagaagac tatgaatgct gtgtactgct tgctacttgt
 500

tgttggttta tggatactgc gatgctttagt ccaagcttagt gtgctttgc atatggtaa
 560

ccaaaacagg attgctaaat ctttagtcgac tgagattaa ccaagtctta gtcaaagcta
 620

241421.txt

tattggcgtg atcttacgta aaaaaaaaaa aaaaaaaaa
658

<210> 16
<211> 122
<212> PRT
<213> Hordeum vulgare

<400> 16

Met Ala Ala Ser Ala Thr Ala Ala Ala Val Ala Ala Glu Val Ile Ser
1 5 10 15

Val His Ser Leu Glu Gln Trp Thr Met Gln Ile Glu Glu Ala Asn Thr
20 25 30

Ala Lys Lys Leu Val Val Ile Asp Phe Thr Ala Ser Trp Cys Gly Pro
35 40 45

Cys Arg Ile Met Ala Pro Val Phe Ala Asp Leu Ala Lys Lys Phe Pro
50 55 60

Asn Ala Val Phe Leu Lys Val Asp Val Asp Glu Leu Lys Pro Ile Ala
65 70 75 80

Glu Gln Phe Ser Val Glu Ala Met Pro Thr Phe Leu Phe Met Lys Glu
85 90 95

Gly Asp Val Lys Asp Arg Val Val Gly Ala Ile Lys Glu Glu Leu Thr
100 105 110

Ala Lys Val Gly Leu His Ala Ala Ala Gln
115 120

<210> 17
<211> 580
<212> DNA
<213> Zea mays

<220>
<221> misc_feature
<223> "n" at position 116, 118, 120, 125, 127, 317, 331, 434, 473,
482,
486, 493, 501, 507, 515, 519, 532, 542, and 579 can be an a, c,
g, or t

<400> 17
tcggatccca caccgaggaa aaggagaaga gagcgcagggt cggaataatg gcggccgagg
60

241421.txt

agggtgccgt gatcgctgc cacaccaagg acgagttcga cgcccgcatg gccaangncn
120

aggancngc aagctggtgg tcatcgactt catggccccc tggtgcaagt ggtgccagat
180

gatggccccc gtgtacgcgg actgcgcagg caagtaccct tccgcggct tcctcgagg
240

cgacgtggac gaactgctgg aagtgcgaa gatctacggc gtccatgtga tgccgacctt
300

ctgcttcatc aggaacngcg agacgctcga nagctttgct accgtcgacg aagacgagct
360

ccgggacgcc gtcaggaagt acgcccgc tggactacg acgctctgc ctggcgtcc
420

gcctaattca gganatgtga tgtgttagcaa atagcgcgcg cgccaccatcg tcnataaata
480

antaantaat aantaattaa ntaantnaag ggccncgtnc aacaacaatt tntggccccc
540

cngtattact acaaatttgc cccccctgtt tcattctgcnt
580

<210> 18
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<212> DNA
<213> Zea mays

<220>
<221> CDS
<222> (60)..(425)

<220>
<221> misc_feature
<223> "n" at position 9, 493, 537, 548, 581, and 584 can be an a, c,
g,
or t

<400> 18
gttgcaatna caacgaacag aagctctcga tctcaccgac accgaggaag aagagatca
59

atg gcg tcc gag cag gga gtc gtg atc gcg tgc cac agc aag gct gag
107
Met Ala Ser Glu Gln Gly Val Val Ile Ala Cys His Ser Lys Ala Glu
1 5 10 15

ttc gac gcc cac atg acc aag gcc cag gaa gcc ggc aag ctg gtg gtc
155
Phe Asp Ala His Met Thr Lys Ala Gln Glu Ala Gly Lys Leu Val Val
20 25 30

241421.txt

atc gac ttc act gcc gcc tgg tgc ggt cca tgc cgc gcc atc gcc cca
203
Ile Asp Phe Thr Ala Ala Trp Cys Gly Pro Cys Arg Ala Ile Ala Pro
35 40 45

ctg ttc gtc gaa cac gcc aag aag ttc act cag gtc gtc ttc ctg aag
251
Leu Phe Val Glu His Ala Lys Lys Phe Thr Gln Val Val Phe Leu Lys
50 55 60

gtg gac gtg gac gaa gtg aag gaa gtc acc gcg gcc tac gag gtc gag
299
Val Asp Val Asp Glu Val Lys Glu Val Thr Ala Ala Tyr Glu Val Glu
65 70 75 80

gcg atg ccg acc ttc cac ttc gtc aag aac ggc aag acg gtc gcg acc
347
Ala Met Pro Thr Phe His Phe Val Lys Asn Gly Lys Thr Val Ala Thr
85 90 95

atc gtg ggt gcc agg aag gac gag ctc ctg gcc cag atc gag aag cat
395
Ile Val Gly Ala Arg Lys Asp Glu Leu Leu Ala Gln Ile Glu Lys His
100 105 110

gcc gcg cct gcg cct gcg tct gcg tct gcc taaaggagat cagtcgtcgc
445
Ala Ala Pro Ala Pro Ala Ser Ala Ser Ala
115 120

cgtcaataag ggccagcacg tatggctgta aatgttgcg ttatcagntc tggctttgtc
505

gtttgtggc gattgtaac tagtagtatg tngttctat ccnaagccgg aggcgatctt
565

aacctggat acttgntng aaaaa
590

<210> 19
<211> 122
<212> PRT
<213> Zea mays

<220>
<221> misc_feature
<223> "n" at position 9, 493, 537, 548, 581, and 584 can be an a, c,
g,
or t

<400> 19

Met Ala Ser Glu Gln Gly Val Val Ile Ala Cys His Ser Lys Ala Glu
1 5 10 15

Phe Asp Ala His Met Thr Lys Ala Gln Glu Ala Gly Lys Leu Val Val
20 25 30

241421.txt

Ile Asp Phe Thr Ala Ala Trp Cys Gly Pro Cys Arg Ala Ile Ala Pro
35 40 45

Leu Phe Val Glu His Ala Lys Lys Phe Thr Gln Val Val Phe Leu Lys
50 55 60

Val Asp Val Asp Glu Val Lys Glu Val Thr Ala Ala Tyr Glu Val Glu
65 70 75 80

Ala Met Pro Thr Phe His Phe Val Lys Asn Gly Lys Thr Val Ala Thr
85 90 95

Ile Val Gly Ala Arg Lys Asp Glu Leu Leu Ala Gln Ile Glu Lys His
100 105 110

Ala Ala Pro Ala Pro Ala Ser Ala Ser Ala
115 120

<210> 20
<211> 948
<212> DNA
<213> Zea mays

<220>
<221> CDS
<222> (3)..(737)

<400> 20
cc aag atc ctc acc gag acc gtc acc acc gtc gac ttc tcc gcc cgc
47
Lys Ile Leu Thr Glu Thr Val Thr Val Asp Phe Ser Ala Arg
1 5 10 15

ccc ttc cgt gtc gcc tcc gac gac acc gtt gtc cac gcc gac tcc gtc
95
Pro Phe Arg Val Ala Ser Asp Asp Thr Val Val His Ala Asp Ser Val
20 25 30

gtc gtc gcc acg ggc gcc gtc gcg cgc agg ctg cac ttc gcc ggc tcc
143
Val Val Ala Thr Gly Ala Val Ala Arg Arg Leu His Phe Ala Gly Ser
35 40 45

gac gcc ttc tgg aac cgg ggc atc tcc gcc tgc gac tgc gac ggg
191
Asp Ala Phe Trp Asn Arg Gly Ile Ser Ala Cys Ala Val Cys Asp Gly
50 55 60

gct gcg cct atc ttc cgg aac aag ccc atc gcc gtc gtc gga ggc ggg
239
Ala Ala Pro Ile Phe Arg Asn Lys Pro Ile Ala Val Val Gly Gly Gly

65

70

75

gac tcc gcc atg gag gag gct aac ttc ctc acc aag tac ggc tcg caa
 287
 Asp Ser Ala Met Glu Glu Ala Asn Phe Leu Thr Lys Tyr Gly Ser Gln
 80 85 90 95

 gtt tac atc atc cac cgc cgc agc gac ttc cgg gcg tcc aag atc atg
 335
 Val Tyr Ile Ile His Arg Arg Ser Asp Phe Arg Ala Ser Lys Ile Met
 100 105 110

 cag gcg cgc acg ctc tcc aac ccc aag atc aag gtc gtc tgg aac tcc
 383
 Gln Ala Arg Thr Leu Ser Asn Pro Lys Ile Lys Val Val Trp Asn Ser
 115 120 125

 gag gtc gtc gag gcc tac ggc ggt gcg gat ggc ggc ccg cta gcc ggc
 431
 Glu Val Val Glu Ala Tyr Gly Gly Ala Asp Gly Gly Pro Leu Ala Gly
 130 135 140

 gtc aag gtc aag gac gtc gtc acc ggc gag gtc tct gat ctc cag gtg
 479
 Val Lys Val Lys Asp Val Val Thr Gly Glu Val Ser Asp Leu Gln Val
 145 150 155

 gcc ggg ctc ttc ttt gcc atc ggt cac gag ccg gcg aca aaa ttt ctt
 527
 Ala Gly Leu Phe Phe Ala Ile Gly His Glu Pro Ala Thr Lys Phe Leu
 160 165 170 175

 gga ggg cag ctc gag ctc gac tct gat ggg tat gtg gtg acc aag ccc
 575
 Gly Gly Gln Leu Glu Leu Asp Ser Asp Gly Tyr Val Val Thr Lys Pro
 180 185 190

 ggt tcc acg cac acc agt gtg cag ggg gtc ttt gca gct ggg gat gtc
 623
 Gly Ser Thr His Thr Ser Val Gln Gly Val Phe Ala Ala Gly Asp Val
 195 200 205

 cag gac aag aag tac cgc cag gcc att act gca gct gga tca ggt tgc
 671
 Gln Asp Lys Lys Tyr Arg Gln Ala Ile Thr Ala Ala Gly Ser Gly Cys
 210 215 220

 atg gct gct ctg gat gca gag cac tac ctg cag gag gtt gga gca cag
 719
 Met Ala Ala Leu Asp Ala Glu His Tyr Leu Gln Glu Val Gly Ala Gln
 225 230 235

 gaa ggg aag acc gat tga ctatgtctgg gccaaagctgc tcttgggcca
 767
 Glu Gly Lys Thr Asp
 240

 agaaaaactt ctccgaaagc cgctctctag tggtgtaaac agcacattat tatttggttt
 827

241421.txt

taggcctcaa attacgttac attggaaatt gatttatatg agcgtgcgca agcttgtata
887

cattattcgc attgtttatt actcttagag tcttagtcat taatcacact ttgctaaaaa
947

a
948

<210> 21
<211> 244
<212> PRT
<213> Zea mays

<400> 21

Lys Ile Leu Thr Glu Thr Val Thr Val Asp Phe Ser Ala Arg Pro
1 5 10 15

Phe Arg Val Ala Ser Asp Asp Thr Val Val His Ala Asp Ser Val Val
20 25 30

Val Ala Thr Gly Ala Val Ala Arg Arg Leu His Phe Ala Gly Ser Asp
35 40 45

Ala Phe Trp Asn Arg Gly Ile Ser Ala Cys Ala Val Cys Asp Gly Ala
50 55 60

Ala Pro Ile Phe Arg Asn Lys Pro Ile Ala Val Val Gly Gly Asp
65 70 75 80

Ser Ala Met Glu Glu Ala Asn Phe Leu Thr Lys Tyr Gly Ser Gln Val
85 90 95

Tyr Ile Ile His Arg Arg Ser Asp Phe Arg Ala Ser Lys Ile Met Gln
100 105 110

Ala Arg Thr Leu Ser Asn Pro Lys Ile Lys Val Val Trp Asn Ser Glu
115 120 125

Val Val Glu Ala Tyr Gly Ala Asp Gly Gly Pro Leu Ala Gly Val
130 135 140

Lys Val Lys Asp Val Val Thr Gly Glu Val Ser Asp Leu Gln Val Ala
145 150 155 160

Gly Leu Phe Phe Ala Ile Gly His Glu Pro Ala Thr Lys Phe Leu Gly

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241421.txt

165

170

175

Gly Gln Leu Glu Leu Asp Ser Asp Gly Tyr Val Val Thr Lys Pro Gly
180 185 190

Ser Thr His Thr Ser Val Gln Gly Val Phe Ala Ala Gly Asp Val Gln
195 200 205

Asp Lys Lys Tyr Arg Gln Ala Ile Thr Ala Ala Gly Ser Gly Cys Met
210 215 220

Ala Ala Leu Asp Ala Glu His Tyr Leu Gln Glu Val Gly Ala Gln Glu
225 230 235 240

Gly Lys Thr Asp

<210> 22
<211> 556
<212> DNA
<213> Zea mays

<220>
<221> CDS
<222> (1)..(336)

<400> 22
ggc ggt gcg gat ggc ggc ccg cta gcc ggc gtc aag gtc aag gac gtc
48
Gly Gly Ala Asp Gly Gly Pro Leu Ala Gly Val Lys Val Lys Asp Val
1 5 10 15

gtc acc ggc gag gtc tct gat ctc cag gtg gcc ggg ctc ttc ttt gcc
96
Val Thr Gly Glu Val Ser Asp Leu Gln Val Ala Gly Leu Phe Phe Ala
20 25 30

atc ggt cac gag ccg gcg aca aaa ttt ctt gga ggg cag ctc gag ctc
144
Ile Gly His Glu Pro Ala Thr Lys Phe Leu Gly Gly Gln Leu Glu Leu
35 40 45

gac tct gat ggg tat gtg gtg ccc aag ccc ggt tcc acg cac acc agt
192
Asp Ser Asp Gly Tyr Val Val Pro Lys Pro Gly Ser Thr His Thr Ser
50 55 60

gtg cag ggg gtc ttt gca gct ggg gat gtc cag gac aag aag tac cgc
240
Val Gln Gly Val Phe Ala Ala Gly Asp Val Gln Asp Lys Lys Tyr Arg
65 70 75 80

cag gcc att act gca gct gga tca ggt tgc atg gct gct ctg gat gca

241421.txt

288

Gln Ala Ile Thr Ala Ala Gly Ser Gly Cys Met Ala Ala Leu Asp Ala
 85 90 95

gag cac tac ctg cag gag gtt gga gca cag gaa ggg aag acc gat tga
 336
 Glu His Tyr Leu Gln Glu Val Gly Ala Gln Glu Gly Lys Thr Asp
 100 105 110

ctatgtctgg gccaaagctgc tcttggccca agaaaaactt ctccgaaagc cgctctctag
 396

tggtgtaaac agcacattat tatttggttt taggcctcaa attacgttac attggaaatt
 456

gatttatatg agcgtgcgca agcttgata cattattcgc attgtttatt actcttagag
 516

tcttagtcat taatcacact ttgctaaaaa aaaaaaaaaa
 556

<210> 23
 <211> 111
 <212> PRT
 <213> Zea mays

<400> 23

Gly Gly Ala Asp Gly Gly Pro Leu Ala Gly Val Lys Val Lys Asp Val
 1 5 10 15

Val Thr Gly Glu Val Ser Asp Leu Gln Val Ala Gly Leu Phe Phe Ala
 20 25 30

Ile Gly His Glu Pro Ala Thr Lys Phe Leu Gly Gly Gln Leu Glu Leu
 35 40 45

Asp Ser Asp Gly Tyr Val Val Pro Lys Pro Gly Ser Thr His Thr Ser
 50 55 60

Val Gln Gly Val Phe Ala Ala Gly Asp Val Gln Asp Lys Lys Tyr Arg
 65 70 75 80

Gln Ala Ile Thr Ala Ala Gly Ser Gly Cys Met Ala Ala Leu Asp Ala
 85 90 95

Glu His Tyr Leu Gln Glu Val Gly Ala Gln Glu Gly Lys Thr Asp
 100 105 110

<210> 24
 <211> 1336

2005-12-04

241421.txt

<212> DNA
<213> Zea mays

<220>

<221> CDS

<222> (91) .. (1086)

<400> 24

gaactgtaat ttcagatttc agagcgcgca agaaccctct tgaccaccgc cgccgcccgc
60gcgaaggccaa gccaaactga gtaaggcagct atg gag gga tcc gcc gcc gct ccg
114Met Glu Gly Ser Ala Ala Ala Pro
1 5ctc cgc acg cgc atc tgc atc atc ggg agc ggt ccc gct gcg cac acg
162Leu Arg Thr Arg Ile Cys Ile Ile Gly Ser Gly Pro Ala Ala His Thr
10 15 20gca gcc atc tac gcg gcc cgc gcg gag ctc aag cct gtg ctc ttc gag
210Ala Ala Ile Tyr Ala Ala Arg Ala Glu Leu Lys Pro Val Leu Phe Glu
25 30 35 40ggc tgg atg gcc aac gac atc gcc gcg ggc ggg cag ctc acc acc acc
258Gly Trp Met Ala Asn Asp Ile Ala Ala Gly Gly Gln Leu Thr Thr Thr
45 50 55acc gac gtc gag aac ttc ccg ggc ttc ccc aac ggc atc atg ggc gcc
306Thr Asp Val Glu Asn Phe Pro Gly Phe Pro Asn Gly Ile Met Gly Ala
60 65 70gac ctc atg gac aac tgc cgc gcg cag tcc ctg cgc ttt ggc acc aac
354Asp Leu Met Asp Asn Cys Arg Ala Gln Ser Leu Arg Phe Gly Thr Asn
75 80 85atc ctc tcc gag acc gtc acc gcc gtc gac ttt tcg gcc tgc cca ttc
402Ile Leu Ser Glu Thr Val Thr Ala Val Asp Phe Ser Ala Cys Pro Phe
90 95 100cga gtt agt gca gac tcc aca acc gtc ctc gcc gat gcg gtt atc gtt
450Arg Val Ser Ala Asp Ser Thr Thr Val Leu Ala Asp Ala Val Ile Val
105 110 115 120gcc acg gga gcc gtc gcg cgg cgc ctc cac ttc ccc ggg tcc gat gca
498Ala Thr Gly Ala Val Ala Arg Arg Leu His Phe Pro Gly Ser Asp Ala
125 130 135tac tgg aac cgc ggc atc tcc gcc tgt gcc gtc tgt gac ggt gcc gcc
546

Tyr Trp Asn Arg Gly Ile Ser Ala Cys Ala Val Cys Asp Gly Ala Ala

241421.txt

140

145

150

ccc atc ttc cgt aac aag ccc atc gcc gtc ata ggc ggc gac tcc
594
Pro Ile Phe Arg Asn Lys Pro Ile Ala Val Ile Gly Gly Asp Ser
155 160 165

gct atg gag gag tcc aat ttc ctc acc aag tac ggc tcc cac gtc tac
642
Ala Met Glu Glu Ser Asn Phe Leu Thr Lys Tyr Gly Ser His Val Tyr
170 175 180

atc atc cac cgc cgc aat acc ttc cgt gct tcc aag atc atg cag gcc
690
Ile Ile His Arg Arg Asn Thr Phe Arg Ala Ser Lys Ile Met Gln Ala
185 190 195 200

agg gcg ctt gag aac ccc aaa att aag gtc ctc tgg gac tcg gaa gtt
738
Arg Ala Leu Glu Asn Pro Lys Ile Lys Val Leu Trp Asp Ser Glu Val
205 210 215

gtc gag gcc tat ggc ggc gca aac ggc ggc cca ttg gct ggc gta aag
786
Val Glu Ala Tyr Gly Gly Ala Asn Gly Pro Leu Ala Gly Val Lys
220 225 230

gtt aag aac cta ctg aat ggt gag gtc tcg gat ctt cag gtg tct ggc
834
Val Lys Asn Leu Leu Asn Gly Glu Val Ser Asp Leu Gln Val Ser Gly
235 240 245

ctc ttc ttc gcc atc ggg cat gag ccg gcg acc aaa ttc ctg ggc gga
882
Leu Phe Phe Ala Ile Gly His Glu Pro Ala Thr Lys Phe Leu Gly Gly
250 255 260

cag ctt gaa ctc gat tca gat ggt tat gtg gaa acc acc aag cca ggt tcc
930
Gln Leu Glu Leu Asp Ser Asp Gly Tyr Val Glu Thr Lys Pro Gly Ser
265 270 275 280

act cac acc agt gta aag ggt gta ttt gct gct ggc gac gtg cag gac
978
Thr His Thr Ser Val Lys Gly Val Phe Ala Ala Gly Asp Val Gln Asp
285 290 295

aag aag tac cgt cag gcc att act gcc gct gga tca ggg tgc atg gct
1026
Lys Lys Tyr Arg Gln Ala Ile Thr Ala Ala Gly Ser Gly Cys Met Ala
300 305 310

gca ttg gac gct gag cac tac ctg cag gag atc ggt gca cag gag gga
1074
Ala Leu Asp Ala Glu His Tyr Leu Gln Glu Ile Gly Ala Gln Glu Gly
315 320 325

aag tct gat tga ctatatttag gtgttagcaac cagcaatcca tcgaatagtc
1126

241421.txt

Lys Ser Asp
330

agttgtcggt gctgaaagcc gctctctgat ggcgcgttat gccatgggtt gtcatgagct
1186

cacgatttagat atacctgatg atttatgctg ctttagtagca tgctattctt atcgtagga
1246

tccagaagta tgtctgaact ctgaactatt tactggatac ctattcgtga ttactgcctt
1306

gaagtttttc ctttagatatac aaaaaaaaaa
1336

<210> 25
<211> 331
<212> PRT
<213> Zea mays

<400> 25

Met Glu Gly Ser Ala Ala Ala Pro Leu Arg Thr Arg Ile Cys Ile Ile
1 5 10 15

Gly Ser Gly Pro Ala Ala His Thr Ala Ala Ile Tyr Ala Ala Arg Ala
20 25 30

Glu Leu Lys Pro Val Leu Phe Glu Gly Trp Met Ala Asn Asp Ile Ala
35 40 45

Ala Gly Gly Gln Leu Thr Thr Thr Asp Val Glu Asn Phe Pro Gly
50 55 60

Phe Pro Asn Gly Ile Met Gly Ala Asp Leu Met Asp Asn Cys Arg Ala
65 70 75 80

Gln Ser Leu Arg Phe Gly Thr Asn Ile Leu Ser Glu Thr Val Thr Ala
85 90 95

Val Asp Phe Ser Ala Cys Pro Phe Arg Val Ser Ala Asp Ser Thr Thr
100 105 110

Val Leu Ala Asp Ala Val Ile Val Ala Thr Gly Ala Val Ala Arg Arg
115 120 125

Leu His Phe Pro Gly Ser Asp Ala Tyr Trp Asn Arg Gly Ile Ser Ala
130 135 140

241421.txt

Cys Ala Val Cys Asp Gly Ala Ala Pro Ile Phe Arg Asn Lys Pro Ile
145 150 155 160

Ala Val Ile Gly Gly Gly Asp Ser Ala Met Glu Glu Ser Asn Phe Leu
 165 170 175

Thr Lys Tyr Gly Ser His Val Tyr Ile Ile His Arg Arg Asn Thr Phe
180 185 190

Arg Ala Ser Lys Ile Met Gln Ala Arg Ala Leu Glu Asn Pro Lys Ile
195 200 205

Lys Val Leu Trp Asp Ser Glu Val Val Glu Ala Tyr Gly Gly Ala Asn
210 215 220

Gly Gly Pro Leu Ala Gly Val Lys Val Lys Asn Leu Leu Asn Gly Glu
225 230 235 240

Val Ser Asp Leu Gln Val Ser Gly Leu Phe Phe Ala Ile Gly His Glu
245 250 255

Pro Ala Thr Lys Phe Leu Gly Gly Gln Leu Glu Leu Asp Ser Asp Gly
260 265 270

Tyr Val Glu Thr Lys Pro Gly Ser Thr His Thr Ser Val Lys Gly Val
 275 280 285

Phe Ala Ala Gly Asp Val Gln Asp Lys Lys Tyr Arg Gln Ala Ile Thr
 290 295 300

Ala Ala Gly Ser Gly Cys Met Ala Ala Leu Asp Ala Glu His Tyr Leu
 305 310 315 320

Gln Glu Ile Gly Ala Gln Glu Gly Lys Ser Asp
325 330